

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,097

DATE: 09/13/2001

TIME: 17:29:08

Input Set : A:\1579-527 seq list.txt

Output Set: N:\CRF3\09132001\I762097.raw

ENTERED

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3 <110> APPLICANT: HERSHFIELD, MICHAEL S.
4     KELLY, SUSAN J.
6 <120> TITLE OF INVENTION: URATE OXIDASE
8 <130> FILE REFERENCE: 1579-379
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/762,097
C--> 11 <141> CURRENT FILING DATE: 2001-08-16
13 <160> NUMBER OF SEQ ID NOS: 11
15 <170> SOFTWARE: PatentIn Ver. 2.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 915
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence ✓
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(915)
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence:PBC CHIMERA ✓
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31 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
32   1             5             10             15
34 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag      96
35 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
36             20             25             30
38 cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa      144
39 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
40             35             40             45
42 ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat      192
43 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
44             50             55             60
46 gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag      240
47 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
48   65             70             75             80
50 ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag      288
51 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
52             85             90             95
54 cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg      336
55 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
56             100            105            110
58 gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc      384
59 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
60             115            120            125
62 cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa      432
63 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
64             130            135            140
66 cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta      480
67 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu

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68 145          150          155          160
70 aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac 528
71 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
72          165          170          175
74 cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa 576
75 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
76          180          185          190
78 gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag 624
79 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
80          195          200          205
82 gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg 672
83 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
84          210          215          220
86 ccc tat gac aaa ggc gag tac tca ccc tct gtg cag aag acc ctc tat 720
87 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
88 225          230          235          240
90 gat atc cag gtg ctc tcc ctg agc cga gtt cct gag atagaa gat atg 768
91 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
92          245          250          255
94 gaa atc agc ctg cca aac att cac tac ttc aat ata gac atg tcc aaa 816
95 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
96          260          265          270
98 atg ggt ctg atc aac aag gaa gag gtc ttg ctg cca tta gac aat cca 864
99 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
100          275          280          285
102 tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912
103 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
104          290          295          300
106 tga 915
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 304
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence:PBC CHIMERA ✓
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119 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
120 1 5 10 15
122 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
123 20 25 30
125 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
126 35 40 45
128 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
129 50 55 60
131 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
132 65 70 75 80
134 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
135 85 90 95
137 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val

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138          100          105          110
140 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
141          115          120          125
143 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
144          130          135          140
146 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
147 145          150          155          160
149 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
150          165          170          175
152 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
153          180          185          190
155 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
156          195          200          205
158 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
159          210          215          220
161 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
162 225          230          235          240
164 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
165          245          250          255
167 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
168          260          265          270
170 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
171          275          280          285
173 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
174          290          295          300
177 <210> SEQ ID NO: 3
178 <211> LENGTH: 915
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <221> NAME/KEY: CDS
184 <222> LOCATION: (1)..(915)
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: pks chimera
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191 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
192 1 5 10 15
194 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag 96
195 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
196 20 25 30
198 cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa 144
199 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
200 35 40 45
202 ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat 192
203 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
204 50 55 60
206 gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag 240
207 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys

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208	65		70		75		80	
210	ttc	aaa	ggc	atc	aaa	agc	ata	gaa
211	Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu
212					85		90	
214	cat	ttc	ctt	tct	tcc	ttc	aag	cat
215	His	Phe	Leu	Ser	Ser	Phe	Lys	His
216					100		105	
218	gaa	gaa	gtt	cct	tgg	aag	cgt	ttt
219	Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe
220					115		120	
222	cat	gca	ttt	att	tat	act	cct	act
223	His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr
224					130		135	
226	cag	ata	agg	aat	gga	cct	cca	gtc
227	Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val
228	145				150		155	
230	aaa	gtc	ttg	aaa	aca	acc	cag	tct
231	Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser
232					165		170	
234	cag	ttc	acc	acc	ctc	cct	gag	gtg
235	Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val
236					180		185	
238	gtg	tac	tgc	aaa	tgg	cgc	tac	cac
239	Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His
240					195		200	
242	gcc	acc	tgg	gac	act	gtt	agg	agc
243	Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser
244					210		215	
246	ccc	tat	gac	aaa	ggc	gag	tac	tcg
247	Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser
248	225				230		235	
250	gac	atc	cag	gtg	ctc	acc	ctg	ggc
251	Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly
252					245		250	
254	gaa	atc	agc	ctg	cca	aat	att	cac
255	Glu	Ile	Ser	Leu	Pro	Asn	Ile	His
256					260		265	
258	atg	gga	ctg	atc	aac	aag	gaa	gag
259	Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu
260					275		280	
262	tat	gga	aaa	att	act	ggt	aca	gtc
263	Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val
264					290		295	
266	tga							
270	<210>	SEQ	ID	NO:	4			
271	<211>	LENGTH:	304					
272	<212>	TYPE:	PRT					
273	<213>	ORGANISM:	Artificial	Sequence				
275	<220>	FEATURE:						

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276 <223> OTHER INFORMATION: Description of Artificial Sequence: pks chimera

278 <400> SEQUENCE: 4

279 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe

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283 20 25 30

285 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln

286 35 40 45

288 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp

289 50 55 60

291 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys

292 65 70 75 80

294 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu

295 85 90 95

297 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val

298 100 105 110

300 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val

301 115 120 125

303 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu

304 130 135 140

306 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu

307 145 150 155 160

309 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp

310 165 170 175

312 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln

313 180 185 190

315 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu

316 195 200 205

318 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly

319 210 215 220

321 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr

322 225 230 235 240

324 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met

325 245 250 255

327 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys

328 260 265 270

330 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro

331 275 280 285

333 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu

334 290 295 300

337 <210> SEQ ID NO: 5

338 <211> LENGTH: 304

339 <212> TYPE: PRT

340 <213> ORGANISM: Artificial Sequence

342 <220> FEATURE:

343 <223> OTHER INFORMATION: Description of Artificial Sequence: baboon D3H

345 <400> SEQUENCE: 5

346 Met Ala His Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe

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